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(54) Title: INCREASING ISOPRENOID BIOSYNTHESIS

(57) Abstract: This invention relates to methods of increasing isoprenoid biosynthesis and/or accumulation, especially in higher plants by genetic manipulation.

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## INCREASING ISOPRENOID BIOSYNTHESIS

This invention relates to methods of modifying plants and, in particular, to methods of increasing isoprenoid biosynthesis and/or accumulation, especially in higher plants and particularly in crop plants. The invention particularly relates to increasing sterol biosynthesis.

The isoprenoids are a large family (> 10,000 members) of compounds with diverse roles in higher plants. They include the sterols, the plant hormones such as the gibberellins and abscisic acid, various components of photosynthetic pigments, the phytoalexins and a variety of other specialised terpenoids. The isoprenoids are of interest to plant biotechnologists because they contribute to various characteristics such as the nutritional quality, flavour, and colour of crop plants and their products, such as fruits and vegetable oils. For example, the carotenoids lycopene and  $\beta$ -carotene are responsible for the colour of tomatoes and carrots respectively.

Isopentenyl diphosphate (IPP), or "isopentyl pyrophosphate", is the precursor of all isoprenoids in eukaryotes. In animals and yeast, it is derived from acetyl-CoA via a biosynthetic pathway in which mevalonic acid, or mevalonate, is an intermediate. In animal cells, the NADPH-dependent reduction of 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) to mevalonic acid is the overall rate-limiting step for the whole sterol biosynthetic pathway. HMG-CoA reductase (3-hydroxy-3-methylglutaryl-CoA reductase or HMGR) is the enzyme which catalyses this step and its activity is regulated through phosphorylation by a protein kinase, adenosine 5' phosphate (AMP) - activated protein kinase, AMPK (Clarke, P.R., and Hardie, D. G., (1990), *EMBO J.* **9**, 2439-2446). It is now clear that AMPK is a homologue of the yeast protein kinase SNF1 and of plant SnRK1s (reviewed by Halford, N. G., and Hardie, D. G., (1998) *Plant Molec Biol* **37**, 735-748). HMGR kinase activities have been partially purified from a number of plant species and there is convincing immunological evidence that the major component of these activities corresponds to the SnRK1 protein kinases (Ball, K. L., *et al*, (1995) *FEBS Lett* **37**, 189-192; Barker J. H. A., *et al*, (1996) *Plant Physiology* **112**, 1141-1149).

Phytosterols are plant sterols and can be divided in three groups based on methylation

levels at C4: 4-desmethylsterols or end product sterols, 4 $\alpha$ -monomethylsterols and 4, 4-di-methylsterols. The major group is the 4-desmethysterols with  $\beta$ -sitosterol, stigmasterol, and campesterol being the most abundant species. Other 4-desmethylsterols found in oilseeds include brassicasterol and  $\Delta^7$ -avenosterol. Phytosterols can occur in free form (free 3 $\beta$ -hydroxyl group) or as conjugates where the 3-hydroxy group is esterified by fatty acids, phenolic acids such as ferulic acid or with sugar moieties. For the purpose of this description the term sterol refers both to free sterols and conjugated sterols.

Mevalonate synthesis via HMGR is also a key step in isoprenoid biosynthesis in plants, although recent evidence suggests the existence of a second pathway for IPP synthesis (Eisenrach W., *et al.*, (1996) *Proc Natl Acad Sci USA* **93**, 6431-6436). In contrast to animal systems, plants contain multiple HMGR genes, the least number found so far being two (HMGR1 and HMGR2) in Arabidopsis (Enjuto M., *et al.*, (1994) *Proc Natl Acad Sci USA* **91**, 927-931). Plant HMGR activity is regulated *in vivo* by reversible phosphorylation of the enzyme (Sipat A. B., (1982) *Phytochemistry* **21**, 2613-2618; Russell D. W., *et al.*, (1985) *Current topics in Plant Biochemistry* (Randall *et al.*, Eds) Columbia MO) as well as transcriptionally (the family members are differentially regulated) (Enjuto M., *et al.*, (1994) *supra*). They have divergent N-terminal domains but highly conserved membrane-insertion sequences and C-terminal catalytic domains (Monfar M., *et al.*, (1990) *Biochemistry of the mevalonic pathway to terpenoids* (Towers, Stafford, Eds) Plenum Press, NY). The catalytic domain of Arabidopsis HMGR1 has been expressed in an active form in *E.coli* bacteria, and inactivated *in vitro* by the partially purified HMGR kinase activity from cauliflower through phosphorylation of serine-577 (Dale S., *et al.*, (1995) *FEBS Lett* **361**, 191-195). This phosphorylation site is present in all of the plant HMGRs characterised so far (See Figure 1, Halford N.G., and Hardie D. G.(1998) *supra*).

The accompanying Fig. 1 (from Halford and Hardie *supra*) shows the regulatory phosphorylation sites on HMG-CoA reductases from different plant species. The residues required for recognition by the SnRK1 family are highlighted as follows: (1) phosphorylated serine (P), bold and underlined; (2) hydrophobic residues at P-5, P+4, bold; (3) basic residues at P-4, underlined. All sequences are from the GENBANK/EMBL databases.

An attempt has been made to upregulate HMGR activity in Arabidopsis by introducing additional copies of HMGR1 under the control of a CaMV35S promoter (Re E. B., *et al*, (1995) *Plant J.* 7, 771-784). As well as increasing the copy number of the gene, this also bypasses the transcriptional regulation of its expression. Although the transcript level was increased 40-fold over the level observed in wild-type plants, HMGR activity increased only 3-fold, and no significant change was seen in the accumulation of isoprenoids. In transgenic tobacco plants expressing a HMGR gene from the rubber plant, *Hevea brasiliensis*, (Schaller H., *et al*, (1995) *Plant Phys* 109, 761-770) and from hamster (Chappell J., *et al*, (1995) *Plant Physiol* 109, 1337-1343), both using the CaMV35S gene promoter, enzyme activity increased 3-8 fold and in these cases sterol production did increase by 3-6 fold. However, observed changes in enzyme activity and sterol content in plants have so far only been reported in leaf tissue, and not in seed tissue.

Although transformed tobacco plants with the sense construction pGGh-1 shared a significant increase in HMGR activity in the plant extract, it was not possible to discriminate whether the increase was due to chimaeric HMGR or to the endogenous tobacco hMGR as a physiological response of the plant (Godoy-Hernandez G. C *et al* (1998) *J. Plant Physiology* 53, 415-424). Also it was not possible to determine whether the alterations in metabolism involved HMGR-related isoprenoid production.

An object of this invention is to increase the levels of isoprenoid, particularly, terpenoid, compounds, and particularly those of nutritional benefit, such as the fat soluble vitamins, like vitamin E and K and sterols, in crop plants and also their products such as rapeseed oil. Both classes of compounds may be efficacious in reducing coronary heart disease. For example, sterols from commonly used edible oils (soybean, rapeseed and sunflower), that is the 4-desmethyl sterols  $\beta$ -sitosterol, stigmasterol, and campesterol, have been shown to have a cholesterol lowering effect (Westrate & Meijer (1998) *Eur J Clin Nutr* 52: 334-344, Jones *et al.* (1997) *Canadian Journal of Physiology and Pharmacology* 75, 217-227; Pelletier *et al.* (1995) *Annals and Nutrition and Metabolism* 39, 291-295) and vitamin E has also been shown to reduce atherosclerotic plaques via oxidation of LDL (Stenvinkel *et al.* (1995) *Kidney International* 5, 1899-1911; Qiao *et al.* (1993) *Arteriosclerosis and thrombosis* 13, 1885-1892). Similarly, vitamin K-dependant proteins, are known to play a regulatory role in vascular biology (Pellegrino *et al.* (1996) *Journal of Pediatric*

*Gastroenterology and Nutrition* **23**, 413-414; Freeman *et al.* (1996) *Journal of Biological Chemistry* **271**, 16227-16236). The proteins are blood coagulation and regulatory proteins that contain  $\gamma$ -carboxyglutamic acid and require calcium for their interaction with cell membranes.  $\gamma$ -carboxyglutamic acid is produced from glutamic acid on the nascent protein chain in a reaction that requires Vitamin K as a cofactor. They include blood clotting factor IX. The data currently suggests that in humans vitamin K-dependent proteins prevent the degeneration of an atherosclerotic vessel wall. In addition, vitamin K is also important in bone metabolism and in the prevention of postmenopausal osteoporosis (Akiyama *et al.* (1999) *Japanese Journal of Pharmacology* **80**, 67-74; Raisz (1999) *Journal of Bone and Mineral Metabolism* **17**, 79-89; Jie *et al.* (1996) *Calcified Tissue International* **59**, 352-356).

The present invention involves introducing novel HMGR genes, in the form of mutant plant and plant/non-plant or different plant chimaeric genes, into plants with the aim of increasing isoprenoid biosynthesis and/or accumulation by uncoupling HMGR from regulation by SnRK1. Transcriptional regulation of the HMGR genes can be avoided by using heterologous promoters. The inventors have shown an increase in seed sterol content, which has not been shown previously.

According to one aspect of the invention there is provided a method of modifying plants. the method comprising modifying a plant HMGR gene which encodes an unmodified HMGR gene product whose activity is regulated so that the modified HMGR gene encodes a modified gene product and placing the modified HMGR gene in a plant or plant cells, in which the modified HMGR gene product is not so regulated.

The unmodified HMGR gene product may be regulated by phosphorylation. Preferably, the modified gene product is no longer subject to regulatory phosphorylation.

The unmodified HMGR gene product may have at least one phosphorylation site. The or each phosphorylation site may include a serine, threonine or tyrosine residue. The or each phosphorylation site may be rendered inactive in the modified HMGR gene product by the replacement of at least one serine, threonine or tyrosine residue of the unmodified gene product with, for example, an alanine residue. Alteration of the phosphorylation site at any

Alternatively, the plant HMGR gene may be modified by the inclusion of a heterologous sequence for a corresponding HMGR gene from another species

In either method, the phosphorylation site may fit the consensus sequence:

Consensus sequence:

<i>Arabidopsis thaliana</i> 1	HM <u>K</u> YNR <u>S</u> SRDI
<i>Camptotheca acuminata</i>	HM <u>K</u> YNR <u>S</u> NKDV
<i>Catharanthus roseus</i>	HM <u>K</u> YNR <u>S</u> SKDI

<i>Hevea brasiliensis</i>	1	HM <u>K</u> YNR <u>S</u> SKDM
<i>Nicotiana glauca</i>		HM <u>K</u> YNR <u>S</u> TKDV
Potato		HM <u>K</u> YNR <u>S</u> IKDI
Rice		HMMYNR <u>S</u> SKDV
Tomato	1	HM <u>K</u> YNR <u>S</u> TKDV

The invention also provides plants and plant reproductive material obtainable by a method of modifying plants according to the invention. The plants may be selected from higher plants such as the crop plants: tobacco, tomatoes, spinach, broccoli, peas, cauliflower and potatoes. Alternatively, the plants may be selected from oil plants such as rapeseed, palm, sunflower, soya bean and tea. The plants may also be selected from monocotyledonous plants, including seeds and the progeny or propagules thereof, for example *Lolium*, *Zea*, *Triticum*, *Sorghum*, *Triticale*, *Bromus*, *Oryzae*, *Avena*, *Hordeum*, *Secale* and *Setaria*, in particular maize, wheat, rice, and barley, as well as dicotyledonous plants, including but not limited to *Fabaceae*, *Brassicaceae*, *Solanum* especially oilseed rape, beans (notably soybeans), sunflower, potatoes, cabbages, spinach, broccoli, peas, cauliflower, tomato, forest trees, roses and tea.

The invention also provides a method of growing plants or plant cells or explants comprising culturing a plant, plant cell, explant or plant reproduction material for example host cultures, obtainable by a method of modifying plants according to the invention. For example, the plant cells and tissue cultures could be made *de novo*, for example by *Agrobacterium tumefaciens*-mediated transformation of plant explants and/or callus culture, or by *Agrobacterium rhizogenes*-mediated transformation of a plant (for example as described by Tepfer D. (1990) *Physiologia Plantarum* 79, 140146) to produce transgenic hairy roots. Plant cells and tissue cultures can also be produced by generating a transgenic plant, as described, and then inducing callus formation by hormone treatment or hairy root formation by *Agrobacterium rhizogenes* infection.

The invention also provides a method of producing isoprenoids comprising culturing a plant or plant cells or explants and collecting isoprenoids for the plant cells or media; and also isoprenoids obtainable by such a method. Isoprenoids obtainable by such a method

include sterols (such as  $\beta$ -sitosterol, campesterol, stigmasterol, brassicasterol and  $\Delta 5$ -avenosterol), terpenoids (such as fat-soluble vitamins) and carotenoids.

The invention also provides seeds obtainable from plants, plant cells and explants and plant reproduction material according to the invention.

The invention further provides a method of producing isoprenoid-containing oil comprising extracting oil from seeds according to the invention.

The invention also provides a nucleotide sequence encoding a modified HMGR, wherein the amino acid sequence of the modified HMGR is altered relative to the amino acid sequence of unmodified HMGR, by amino acid substitution of at least one serine, threonine or tyrosine residue at a phosphorylation site within the HMGR.

The invention further provides a method for increasing pathogen, fungus and insect and mite pest resistance in plants by increasing the expression of an isoprenoid in the plant by modifying the plant as defined above. Examples of such fungus are *Fusarium*, *Aspergillus*, *Phytophthora*, *Gaeumannomyces*, Downy mildews, *Colletotrichum*, *Cochliobolus*, *Tapesia*, *Magnaporthe*, *Stagonospora*, *Rhynchosporium*, *Septoria*, *Helminthosporium*, and powdery mildews such as *Blumeria* and *Erysiphe*. Examples of insect and mite pests are Homoptera, Diptera, Lepidoptera, Coleoptera, Hemiptera, Hymenoptera, Dictyoptera, Orthoptera, arachnids and mites. The method may also include attracting beneficial species of insects and mites such as any species of Hymenoptera, Odonata, Hemiptera, Coleoptera, Neuroptera, and arachnids including spiders and predatory mite, or their larvae.

The invention also provides a nucleotide sequence encoding a chimaeric HMGR comprising an N-terminal domain-encoding region derived from a plant HMGR nucleotide sequence, and a C-terminal domain-encoding region HMGR nucleotide sequence derived from a different organism, such as a yeast.



The nucleotide sequence may comprise a heterologous promoter such as CaMV35S or ACP.

The invention also provides a HMGR encoded by a nucleotide sequence according to the invention.

The invention further provides a method of increasing the levels of 4-desmethylsterols in plants and seeds by expression of a HMGR according to the invention.

Two particular strategies to produce novel modified HMGR enzymes that are uncoupled from phosphorylation control can be used.

The first strategy involves site directed mutagenesis of the active serine in the enzyme, thereby removing the target for the SnRK1s which phosphorylate the unmodified enzyme.

For example, the sequence of Arabidopsis HMGR1 that encodes Ser<sup>577</sup> can be altered for example from TCC to GCC, which encodes Ala.

The second strategy involves the construction of a chimaeric gene comprising the catalytic domain-encoding region of an HMGR gene from another isoprenoid-synthesizing organism, for example the yeast HMGR gene, and the N-terminal domain-encoding region of Arabidopsis HMGR1. The gene can then be produced by PCR amplification of the N-terminal region of Arabidopsis HMGR1, which should ensure that the chimaeric HMGR protein is targeted to the correct location in the plant cell and the C-terminal region of yeast HMGR using primers which incorporate a suitable restriction site at the "join", and ligation and cloning of the PCR products. The fusion point is preferably located at the C-terminal end of the linker region between the membrane-spanning domain and the catalytic domain. Other fusions are contemplated and are within the ambit of the skilled worker.

These novel HMGR sequences can be placed in vectors downstream of the constitutive CaMV35S (Odell J. T., *et al*, (1985) *Nature* **313**, 810-812) and acyl carrier protein (ACP) promoters. The ACP promoter De Silva J., *et al*, (1992) *Plant Molec Biol* **18**, 1163-1172 WO92/18634) is active only in seed ("seed specific" - Gallie, D. R., *et al* (1989) *Plant Cell*

1, 301-311; promoters and introduced into tobacco and oilseed rape plants. A suitable ACP promoter-containing vector is pNH12. A suitable CaMV35S promoter containing vector is pJD330. The use of heterologous promoters avoids the transcriptional regulation of the HMGR gene which occurs with the unmodified gene.

The generation of plants and plant tissues in accordance with the invention will now be described, by way of example only, with reference to the following further drawings Figures 2 to 6 in which:

Fig. 2 shows the nucleotide and derived amino acid sequence of *S. cerevisiae* HMG-CoA reductase gene HMGR1 (EMBL database accession number M22002);

Fig. 3 shows the nucleotide and derived amino acid sequence of Arabidopsis HMG-CoA reductase gene HMGR1 (EMBL database accession number J04537);

Fig. 4a shows a schematic diagram of the construction of genes comprising the acyl carrier protein (ACP) gene promoter, nopaline synthase gene terminator (terminator) and either the mutant arabidopsis HMGR1 containing the T1799-G (Serine577-alanine) substitution or the chimaeric arabidopsis/yeast HMGR gene.

Fig. 4b shows a schematic diagram of the construction of genes comprising the CaMV35S gene promoter,  $\Omega$  enhancer sequence ( $\Omega$ ), nopaline synthase gene terminator (terminator) and either the mutant arabidopsis HMGR1 containing the T1799-G (Serine577-alanine) substitution, or the chimaeric arabidopsis/yeast HMGR gene.

Fig. 5A shows a ATHMGRM sequence (i.e. mutant ATHMGR1 sequence) and Fig. 5B shows a chimeric HMGR1 sequence used in constructs of the invention; and

Fig. 6 is an alignment of derived amino acid sequences of HMG-CoA reductases encoded by wild type Arabidopsis gene, HMGR1 (athmgr1), a novel mutant gene, (athmgrm) in which the serine residue (S) at position 577 is replaced with an alanine residue (A), part of the yeast (*Saccharomyces cerevisiae*) wild type gene (schmgr1) and a novel chimaeric gene comprising the N-terminal membrane-spanning part of the Arabidopsis HMGR1 gene and the C-terminal catalytic part of the yeast HMGR1 gene. Matching residues are highlighted with a black background. Residue numbers are given on the right.

Fig. 7 is an alignment of derived amino acid sequences of HMG-CoA reductases encoded by wild type Arabidopsis gene, HMGR1 (*athmgr1*) and the mutant gene, (*athmgrm*) in which the serine residue (S) at position 577 is replaced with an alanine residue (A). Matching residues are highlighted with a black background.

Fig. 8 is an alignment of derived amino acid sequences of HMG-CoA reductases encoded by wild type Arabidopsis gene, HMGR1 (*athmgr1*), yeast (*Saccharomyces cerevisiae*) wild type gene (*schmgr1*) and a novel chimaeric gene comprising the N-terminal membrane-spanning part of the Arabidopsis HMGR1 gene and the C-terminal catalytic part of the yeast HMGR1 gene. For clarity, only the N-terminal portion of the Arabidopsis protein and C-terminal portion of the yeast protein are included, but all of the novel chimaeric protein is shown. Matching residues are highlighted with a black background. Residue numbers are given on the right.

Fig. 9 is a bar chart comparing levels of EJD25 and MAS1 sterols in leaf material.

Fig. 10 is a bar chart comparing levels EJD25, ENH7 and MAS1 sterols in seed material.

## 1. Generation of engineered plants

Modified plants can be produced according to two strategies: either the HMGR gene is modified by site directed mutagenesis so as to encode a modified gene product which is resistant to phosphorylation because it lacks a specific serine residue (serine 577) or a more substantial modification is made to the HMGR gene so that a C terminal portion in the HMGR gene product is replaced by a coding region from a different organism.

### a. Site directed mutagenesis of HMGR gene

Primers ATACAATAGAGCCAGCCGAGAC and GTCTCGGCTGGCTCTATTGTAT are generated and used for site-directed mutagenesis (for example using Stratagene Quickchange system) of the ATHMGR1 sequence to replace T<sup>1799</sup> with G, causing a Serine<sup>577</sup> to alanine substitution in the encoded protein (See Fig. 5A). Alterations may be also performed to cause substitutions at positions 572, 573, 574 or 581 of the amino acid sequence, corresponding to the positions highlighted in Figure. 1.

The modified gene, ATHMGRM, is shown schematically in Fig. 4 and its sequence is shown in Fig. 5. A. The modified HMGR1 coding sequence is under the control of the ACP promoter. The terminator is the nopaline synthase (nos) termination sequence. The modified HMGR gene is then introduced into plants using conventional *Agrobacterium tumefaciens* - mediated transformation (Bevan, M, 1984 *infra*).

**b. Production of chimaeric HMGR genes**

ATHMGR1 sequences can be amplified from Arabidopsis total RNA by rtPCR.

SCHMGR1 sequences are amplified from yeast total RNA by rtPCR. The following oligonucleotide primers can be used:

1. ACGTCCATGGATCTCCGTCGGAGGC

2. ACGTGAATTCAGATTCAGATCATGT

This pair are used to amplify the full-length ATHMGR1 sequence (71 – 1858 in the sequence of Figure 3 below) and to incorporate *Nco*I and *Eco*RI restriction sites

3. AAACCTGCAGAGAAACAAAGAGGTCGCC

4. ACGTGAATTCGACGTATGACTAAGTTTAGG

are used to amplify the catalytic domain of SCHMGR1 (encoded by base pairs 1970 - 3298 in sequence below) and to incorporate *Pst*I and *Eco*RI restriction sites within the amplified DNA.

5. GTCTTCTGCAGGAAGCGATTCCGGT

This oligonucleotide together with oligonucleotide ACGTCCATGGATCTCCGTCGGAGGC can be used to amplify the targeting domain of AtHMGR1 (71 – 578 below)

Two additional constructs can be made by cloning the mutant and chimaeric HMGR sequences downstream of an  $\Omega$ -enhanced CaMV35S promoter in plasmid PJD330 (Gallie, D. R., *et al* (1989) *supra*). This promoter drives expression in a constitutive manner. This

involves amplification of the sequences with the original 5' oligonucleotides and the following 3' oligonucleotides:

Mutant arabidopsis HMGR:

ACGTCCCGGGAGATTCAGATCATGT

Chimaeric HMGR:

ACGTCCCGGGACGTATGACTAAGTTTAGGA

These will introduce a SmaI site at the 3' end (see Fig. 4b).

The resulting constructs are then introduced into plants as described above.

Mutant and chimaeric HMGR genes have been produced. The mutant gene was produced by converting T<sup>1799</sup> (Fig. 3) of the *Arabidopsis* gene to a G, by site directed mutagenesis, leading to a Serine to Alanine substitution in the SnRK phosphorylation site. This should remove the encoded protein from phosphorylational control by the kinase. The chimaeric gene was prepared by joining the targeting domain of the Arabidopsis gene to the catalytic domain of the yeast gene and lacks the SNF1/SnRK1 phosphorylation site. The HMGR protein is not under the control of the Snf1 kinase in yeast. The entire nucleotide sequences of these genes have been checked against those published. The sequences have been placed downstream of cauliflower mosaic virus 35S RNA and ACP promoters by cloning them into JD330 and NH12 plasmids respectively, to make a total of 4 chimaeric gene constructs, 35S-mutant HMGR (MAS), 35S-chimaeric HMGR (ASS), ACP-mutant HMGR (MAE) and ACP-chimaeric HMGR (MASE).

**c. Plasmids containing the chimaeric gene constructs have been used to transform tobacco (SR1) using Agrobacterium-mediated transformation.** Control plants have been produced containing promoter and terminator sequences without the HMGR inserts. The numbers of transgenic plants generated is given in Table 1:

**Table 1**

Construct	Number of Plant
35S-mutant HMGR	33

35S-chimaeric HMGR	24
35S-empty cassette	21
ACP-mutant HMGR	44
ACP-chimaeric HMGR	18
ACP-empty cassetts	11

The transgenic plants have been analysed by RT-PCR, measurement of HMGR activity, and also analysis of sterol content. 16 plants have been analysed for sterol content and at least one, MAS1, containing the 35S mutant HMGR construct has been found to have a higher sterol content than controls in both leaves and seeds. Analyses of its sterol content compared with EJD25 (35S - empty cassettes) and ENH7 (ACP-empty cassettes) are shown in Figs. 9 and 10.

The inventors have shown that transforming a plant with an HMGR gene encoding a protein lacking in the target phosphorylation site recognized by the SnRK1 protein kinase results in increased sterol biosynthesis.

#### d. Production of other plants which have been engineered

Other plants such as oilseed rape can be produced by transformation using *Agrobacterium tumefaciens* (See Bevan M. *Nucl. Acids Res.* 1984; **12**, 8711-8721; Horsch, R. B., (1985) *Science* **227**, 1229-1231).

## 2. Generation of plant cells

### a. Production of engineered tobacco cells

Plant cells can be produced from the plants described in Example 1 above or they could be made *de novo*, for example by *Agrobacterium tumefaciens*-mediated transformation of a callus culture, or by *Agrobacterium rhizogenes*-mediated transformation of a plant (for example as described in Tepfer, D. (1990) *Physiologia Plantarum* **79**: 140-146) to produce hairy roots. Alternatively, plant and tissue cultures can be generated by producing a transgenic plant, as described, then inducing callus formation by hormone treatment or hairy root formation by *Agrobacterium rhizogenes* infection. Calluses can be produced as described for example by Mar *et al* (1997) *Plant Molecular Biology* **34**, 31-43 with the technique being adapted by the skilled worker. Generally, calluses can be induced from

many different plant tissues by treatment with an auxin (usually 2,4-dichlorophenoxyacetic acid).

The production of isoprenoids in hairy root cultures is well known. Examples of isoprenoid production in hairy root cultures are given by: Sim, S. J. *et al* (1994), *Journal of Fermentation and Bioengineering* **78**, 229-234; Takeda, T. *et al* (1994) *Chem. Pharm. Bull.* **42**, 730-732; Delbecque *et al* (1995) *Eur. J. Entomol.* **92**, 301-307; Hu, Z-B. and Alferman, A. W. (1993) *Phytochemistry* **32**, 699-703; and Sato K. *et al* (1991) *Phytochemistry* **30**, 1507-1510 by way of example.

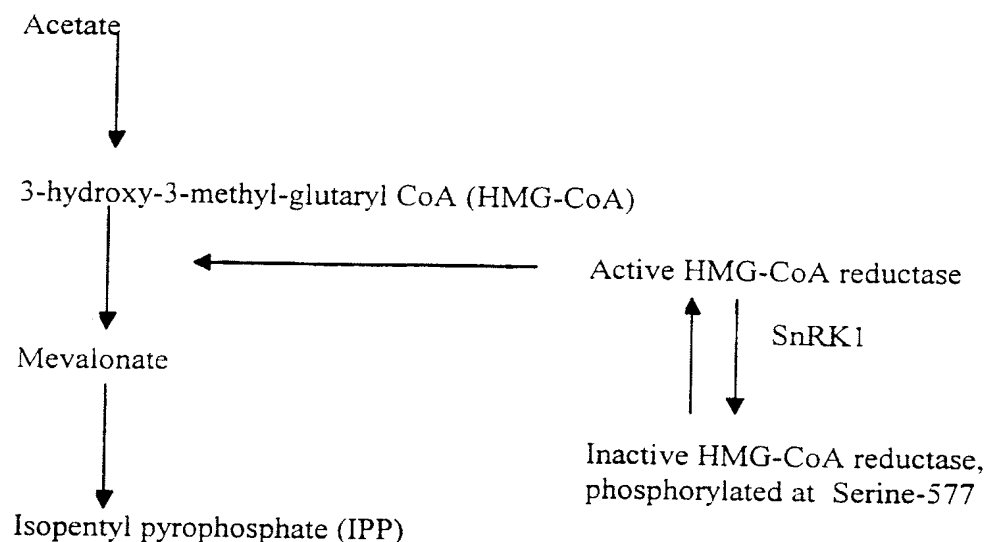
#### **b. Culture of plant cells**

Plant cells produced as described above can be cultured under normal conditions.

#### **3. Production of isoprenoids.**

Plants and plant cells and explants produced as described above were grown under normal conditions and HMGR activity measured by the radiochemical method described by Chappell *et al.* (1995) (*Plant Physiology* **109**, 1337-1343). Sterol content was analysed by gas chromatography-mass spectroscopy (gc-ms)

A schematic representation of the preparation of isopentyl pyrophosphate is shown in the following flow diagram:

**Flow diagram**

IPP is the precursor of all isoprenoids, including sterols, gibberellins, ABA, phytoalexins, various pigments, carotenoids, fat-soluble vitamins (e.g E and K) and more.

Whilst the invention has been described in relation to increasing isoprenoids in oilseeds to enhance the value of the oil, the invention can be used to improve food quality or nutritional value of many crops. Other applications include increasing pathogen and insect resistance of plants, and in the production of pharmaceuticals, fragrances and other non-food substances in plants and plant callus or cell or explant cultures.



**Claims**

1. A method of modifying plants, the method comprising modifying a plant HMGR gene which encodes an unmodified HMGR gene product whose activity is regulated so that the modified HMGR gene encodes a modified HMGR gene product, and placing the modified HMGR gene in a plant or plant cells, in which the modified HMGR gene product is not so regulated.
2. A method according to claim 1 in which the unmodified HMGR gene product is regulated by phosphorylation.
3. A method according to claim 1 or 2 in which the modified HMGR gene product is no longer subject to regulatory phosphorylation.
4. A method according to claim 1, 2 or 3 in which the unmodified HMGR gene product has at least one phosphorylation site.
5. A method according to claim 4 in which the or each phosphorylation site includes a serine, threonine or tyrosine residue.
6. A method according to claim 5 in which the phosphorylation site has been rendered inactive in the modified HMGR gene product by the replacement of at least one serine threonine or tyrosine residue of the unmodified gene product.
7. A method according to claim 6 in which at least one serine, threonine or tyrosine residue is replaced by at least one alanine or other residue.
8. A method according to any preceding claim in which the HMGR gene is modified to reduce transcriptional regulation.
9. A method according to claim 8 in which the HMGR gene is modified through the introduction of at least one heterologous promoter.

10. A method according to claim 9 in which the heterologous promoter is selected from the CaMV35S and ACP promoters.
11. A method according to claim 9 wherein the ACP promoter is a rapeseed ACP promoter.
12. A method according to claim 1 in which the method comprises modifying a plant HMGR gene which encodes an unmodified HMGR gene product whose activity is regulated, by the inclusion of a heterologous sequence for a corresponding HMGR gene from another species.
13. A method according to claim 12 in which the heterologous sequence is derived from another plant species, yeast or fungi or another isoprenoid-producing organism.
14. A method according to claim 12 or 13 and in which the heterologous sequence is derived from a yeast, in which the yeast is selected from *S. cerevisiae*, *S. pombe* and *Candida* spp.
15. A method according to any one of claims 4 to 7 in which the phosphorylation site fits the consensus sequence:

	-5	-3	↓	+4
Consensus sequence:	XMXRXXSXXXL			
	L	K	T	F
	V	H		I
	FRX			M
	I			V

16. A method according to claim 15 wherein the phosphorylation site is selected from:

<i>Arabidopsis thaliana</i> 1	HM <u>K</u> YNR <u>S</u> SRDI
<i>Camptotheca acuminata</i>	HM <u>K</u> YNR <u>S</u> NKDV
<i>Catharanthus roseus</i>	HM <u>K</u> YNR <u>S</u> SKDI

<i>Hevea brasiliensis</i> 1	HM <u>K</u> YNR <u>S</u> SKDM
<i>Nicotiana sylvestris</i>	HM <u>K</u> YNR <u>S</u> TKDV
Potato	HM <u>K</u> YNR <u>S</u> IKDI
Rice	HM <u>M</u> YNR <u>S</u> SKDV
Tomato 1	HM <u>K</u> YNR <u>S</u> TKDV

17. A method according to any one of claims 1 to 16 in which the plant is selected from higher plants.
18. A method according to claim 17 in which the higher plant is a crop plant.
19. A method according to claim 18 in which the crop plant is selected from tobacco, tomatoes, vegetables such as spinach, broccoli, peas cauliflower and potatoes, oil plants such as rapeseed, palm, sunflower, soybean, tea, maize, wheat, rice, barley, beans, sunflower, cabbage, tomato, forest trees and roses.
20. Plants, plant cells and explants and plant reproductive material obtainable by a method according to any preceding claim.
21. A method of growing plants or plant cells or explants comprising culturing a plant, plant cell, explant or plant reproduction material according to claim 20.
22. A method of producing isoprenoids comprising culturing a plant, plant cell or explant according to claim 20 and collecting isoprenoids from the plant, plant cell or explant or media.
23. A method according to claim 22 in which the plant is selected from higher plants.
24. A method according to claim 23 in which the higher plant is a crop plant.

25. A method according to claim 24 in which the crop plant is selected from tobacco, tomatoes, vegetables such as spinach, broccoli, peas, cauliflower and potatoes, oil plants such as rapeseed, palm, sunflower, soybean, tea, maize, wheat, rice, barley, beans, sunflower, cabbage, forest trees and roses.
26. A method according to any one of claims 22 to 25 in which the isoprenoid is a sterol, a terpenoid or a carotenoid.
27. A method according to any one of claims 22 to 26 in which the isoprenoid is a fat soluble vitamin.
28. A method according to claim 26 and in which the isoprenoid is a sterol in which the sterol is  $\beta$ -sitosterol, campesterol, stigmasterol, brassicasterol or  $\Delta^5$ -avenosterol.
29. Isoprenoids obtainable by a method according to any one of claims 22 to 25.
30. Seeds obtained from plants, plant cells and explants and plant reproductive material according to claim 20.
31. A method of producing isoprenoid-containing oil comprising extracting the oil from seeds according to claim 30.
32. A nucleotide sequence encoding a modified HMGR, wherein the amino acid sequence of the modified HMGR is altered relative to the amino acid sequence of unmodified HMGR by amino acid substitution of at least one serine, threonine or tyrosine residue at a phosphorylation site within the HMGR.
33. A nucleotide sequence encoding a chimaeric HMGR comprising an N-terminal domain-encoding region derived from a plant HMGR nucleotide sequence, and a C-terminal domain-encoding region HMGR nucleotide sequence derived from a different organism.

34. A nucleotide sequence according to claim 33 wherein the different organism is a yeast.
35. A nucleotide sequence according to any one of claims 32 to 34 comprising a heterologous promoter.
36. A nucleotide sequence according to claim 35 wherein the heterologous promoter is CaMV355 or ACP.
37. A HMGR encoded by a nucleotide sequence according to any one of claims 32 to 36.
38. A method of increasing the levels of 4-desmethylsterols in plants and seeds by expression of a HMGR according to claim 37.
39. A method of increasing pathogen resistance in a plant, the method comprising increasing expression of an isoprenoid in the plant by a method of modifying the plant according to any one of claims 1 to 19.
40. A method according to claim 39 in which the plant is selected from monocotyledonous plants, including seeds and the progeny or propagules thereof, for example *Lolium*, *Zea*, *Triticum*, *Sorghum*, *Triticale*, *Bromus*, *Oryzae*, *Avena*, *Hordeum*, *Secale* and *Setaria*, in particular maize, wheat, rice, and barley, as well as dicotyledonous plants, including but not limited to *Fabaceae*, *Brassicaceae*, *Solanum* especially oilseed rape, beans (notably soybeans), sunflower, potatoes, cabbages, spinach, broccoli, peas, cauliflower, tomato, forest trees, roses and tea.
41. A method according to claim 39 in which the pathogen is a fungus.
42. A method according to claim 41 in which the fungus is any species of *Fusarium*, *Aspergillus*, *Phytophthora*, *Gaeumannomyces*, Downy mildews, *Colletotrichum*, *Cochliobolus*, *Tapesia*, *Magnaporthe*, *Stagonospora*, *Rhynchosporium*, *Septoria*, *Helminthosporium*, and powdery mildews such as *Blumeria* and *Erysiphe*.

43. A method of increasing resistance to insect and mite pests in a plant, the method comprising increasing expression of an isoprenoid in the plant by a method of modifying the plant according to any one of claims 1 to 19.
44. A method according to claim 43 in which the insect is any species of Homoptera, Diptera, Lepidoptera, Coleoptera, Hemiptera, Hymenoptera, Dictyoptera, Orthoptera, arachnids and mites.
45. A method according to claim 43 in which a beneficial insect or a mite, such as any species of Hymenoptera, Odonata, Hemiptera, Coleoptera, Neuroptera, and arachnids including spiders and predatory mite, or their larvae is attracted to the plant.

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<i>Arabidopsis thaliana</i> 1	HM <u>K</u> YNR <u>S</u> SRDI
<i>Camptotheca acuminata</i>	HM <u>K</u> YNR <u>S</u> NKDV
<i>Catharanthus roseus</i>	HM <u>K</u> YNR <u>S</u> SKDI
<i>Hevea brasiliensis</i> 1	HM <u>K</u> YNR <u>S</u> SKDM
<i>Nicotiana sylvestris</i>	HM <u>K</u> YNR <u>S</u> TKDV
Potato	HM <u>K</u> YNR <u>S</u> IKDI
Rice	HMMYNR <u>S</u> SKDV
Tomato 1	HM <u>K</u> YNR <u>S</u> TKDV

FIG. 1

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## FIG. 2

Yeast HMGR1

1	TTTATTAACCTTATTTTTTTCTTCTTTCTACCCAATTCTAGTCAGGAAAAGACTAAGGGCT	60
61	GGAACATAGTGTATCATTGTCTAATTGTTGATACAAAGTAGATAAATACATAAAACAAGC	120
121	M P P L F K G L K Q M A K P I A Y V S R ATGCCGCCGCTATTCAAGGGACTGAAACAGATGGCAAAGCCAATTGCCTATGTTTCAAGA	180
181	F S A K R P I H I I L F S L I I S A F A TTTTCGGCGAAACGACCAATTCAATATAACTTTTTTCTCTAATCATATCCGCATTTCGCT	240
241	Y L S V I Q Y Y F N G W Q L D S N S V F TATCTATCCGTCATTCACTATTACTTCAATGGTTGGCAACTAGATTCAAATAGTGTTTTT	300
301	E T A P N K D S N T L F Q E C S H Y Y R GAAACTGCTCCAAATAAAGACTCCAACACTCTATTTCAAGAATGTTCCCATTACTACAGA	360
361	D S S L D G W V S I T A H E A S E L P A GATTCCTCTCTAGATGGTTGGGTATCAATCACCGCGCATGAAGCTAGTGAGTTACCAGCC	420
421	P H H Y Y L L N L N F N S P N E T D S I CCACACCATTACTATCTATTAACCTGAACTTCAATAGTCCTAATGAAACTGACTCCATT	480
481	P E L A N T V F E K D N T K Y I L Q E D CCAGAAGTAGCTAACACGGTTTTTGGAGAAAGATAATACAAAATATATTCTGCAAGAAGAT	540
541	L S V S K E I S S T D G T K W R L R S D CTCAGTGTTCCTCAAAGAAATTTCTTCTACTGATGGAACGAAATGGAGGTTAAGAAGTGAC	600
601	R K S L F D V K T L A Y S L Y D V F S E AGAAAAAGTCTTTTCGACGTAAAGACGTTAGCATATTCTCTCTACGATGTATTTTCAGAA	660
661	N V T Q A D P F D V L I M V T A Y L M M AATGTAACCCAAGCAGACCCGTTTGACGTCCTTATTATGGTTACTGCCTACCTAATGATG	720
721	F Y T I F G L F N D M R K T G S N F W L TTCTACACCATATTTCGGCCTCTTCAATGACATGAGGAAGACCGGGTCAAATTTTTGGTTG	780
781	S A S T V V N S A S S L F L A L Y V T Q AGCGCCTCTACAGTGGTCAATTCTGCATCATCACTTTTCTTAGCATTGTATGTCACCCAA	840
841	C I L G K E V S A L T L F E G L P F I V TGTATTCTAGGCAAAGAAGTTTCCGCATTAACTCTTTTGAAGGTTTGCCTTTTCATTGTA	900
901	V V V G F K H K I K I A Q Y A L E K F E GTTGTTGTTGGTTTCAAGCACAAAATCAAGATTGCCAGTATGCCCTGGAGAAATTTGAA	960
961	R V G L S K R I T T D E I V F E S V S E AGAGTCGGTTTATCTAAAAGGATTACTACCGATGAAATCGTTTTTGAATCCGTGAGCGAA	1020
1021	E G G R L I Q D H L L C I F A F I G C S GAGGGTGGTCGTTTGATTCAAGACCATTGCTTTGTATTTTTGCCTTTATCGGATGCTCT	1080
1081	M Y A H Q L K T L T N F C I L S A F I L ATGTATGCTCACCAATTGAAGACTTTGACAAACTTCTGCATATTATCAGCATTTATCCTA	1140

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1141 I F E L I L T P T F Y S A I L A L R L E 1200  
ATTTTGAATTGATTTTAACTCCTACATTTTATTCTGCTATCTTAGCGCTTAGACTGGAA

1201 M N V I H R S T I I K Q T L E E D G V V 1260  
ATGAATGTTATCCACAGATCTACTATTATCAAGCAAACATTAGAAGAAGACGGTGTGTGTT

1261 P S T A R I I S K A E K K S V S S F L N 1320  
CCATCTACAGCAAGAATCATTCTTAAAGCAGAAAAGAAATCCGTATCTTCTTTCTTAAAT

1321 L S V V V I I M K L S V I L L F V F I N 1380  
CTCAGTGTGGTTGTCATTATCATGAACTCTCTGTCATACTGTTGTTTGTCTTCATCAAC

1381 F Y N F G A N W V N D A F N S L Y F D K 1440  
TTTTATAACTTTGGTGCAAATTGGGTCAATGATGCCTTCAATTCATTGTACTTCGATAAG

1441 E R V S L P D F I T S N A S E N F K E Q 1500  
GAACGTGTTTCTCTACCAGATTTTATTACCTCGAATGCCTCTGAAAACCTTAAAGAGCAA

1501 A I V S V T P L L Y Y K P I K S Y Q R I 1560  
GCTATTGTTAGTGTCACCCCATTTATTATATTACAAACCCATTAAGTCCTACCAACGCATT

1561 E D M V L L L L R N V S V A I R D R F V 1620  
GAGGATATGGTTCTTCTATTGCTTCGTAATGTCAGTGTGCCATTTCGTGATAGGTTTCGTC

1621 S K L V L S A L V C S A V I N V Y L L N 1680  
AGTAAATTAGTTCTTTCGCGCTTAGTATGCAGTGCTGTCATCAATGTGTATTTATTGAAT

1681 A A R I H T S Y T A D Q L V K T E V T K 1740  
GCTGCTAGAATTCATACCAGTTATACTGCAGACCAATTGGTGAAAACCTGAAGTCACCAAG

1741 K S F T A P V Q K A S T P V L T N K T V 1800  
AAGTCTTTTACTGCTCCTGTACAAAAGGCTTCTACACCAGTTTTTAACCAATAAAACAGTC

1801 I S G S K V K S L S S A Q S S S S G P S 1860  
ATTTCTGGATCGAAAGTCAAAAGTTTATCATCTGCGCAATCGAGCTCATCAGGACCTTCA

1861 S S S E E D D S R D I E S L D K K I R P 1920  
TCATCTAGTGAGGAAGATGATTCCCGCGATATTGAAAGCTTGGATAAGAAAATACGTCCT

1921 L E E L E A L L S S G N T K Q L K N K E 1980  
TTAGAAGAATTAGAAGCATTATTAAGTAGTGGAATAACAAAACAATTGAAGAACAAAGAG

1981 V A A L V I H G K L P L Y A L E K K L G 2040  
GTCGCTGCCTTGGTTATTCACGGTAAGTTACCTTTGTACGCTTTGGAGAAAAAATTAGGT

2041 D T T R A V A V R R K A L S I L A E A P 2100  
GATACTACGAGAGCGGTTGCGGTACGTAGGAAGGCTCTTTCAATTTTGGCAGAAGCTCCT

2101 V L A S D R L P Y K N Y D Y D R V F G A 2160  
GTATTAGCATCTGATCGTTTACCATATAAAAATTATGACTACGACCGGTATTTGGCGCT

2161 C C E N V I G Y M P L P V G V I G P L V 2220  
TGTTGTGAAAATGTTATAGGTTACATGCCTTTGCCCCGTTGGTGTATAGGCCCTTGGTT

2221 I D G T S Y H I P M A T T E G C L V A S 2280  
ATCGATGGTACATCTTATCATATACCAATGGCAACTACAGAGGTTGTTTGGTAGCTTCT

2281 A M R G C K A I N A G G G A T T V L T K 2340  
GCCATGCGTGGCTGTAAGGCAATCAATGCTGGCGGTGGTGCAACAACCTGTTTTAACTAAG

FIG. 2CONT'D

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D G M T R G P V V R F P T L K R S G A C  
2341 GATGGTATGACAAGAGGCCAGTAGTCCGTTTCCCACTTTGAAAAGATCTGGTGCCTGT 2400

K I W L D S E E G Q N A I K K A F N S T  
2401 AAGATATGGTTAGACTCAGAAGAGGGACAAAACGCAATTAAAAAGCTTTTAACTCTACA 2460

S R F A R L Q H I Q T C L A G D L L F M  
2461 TCAAGATTTGCACGTCTGCAACATATTCAAACCTTGTCTAGCAGGAGATTTACTCTTCATG 2520

R F R T T T G D A M G M N M I S K G V E  
2521 AGATTTAGAACAACACTACTGGTGACGCAATGGGTATGAATATGATTTCTAAAGGTGTGCGAA 2580

Y S L K Q M V E E Y G W E D M E V V S V  
2581 TACTCATTAAGCAAATGGTAGAAGAGTATGGCTGGGAAGATATGGAGGTTGTCTCCGTT 2640

S G N Y C T D K K P A A I N W I E G R G  
2641 TCTGGTAACTACTGTACCGACAAAAAACCAGCTGCCATCAACTGGATCGAAGGTCGTGGT 2700

K S V V A E A T I P G D V V R K V L K S  
2701 AAGAGTGTCTGCGCAGAAGCTACTATTCTGGTGATGTTGTCAGAAAAGTGTTAAAAAGT 2760

D V S A L V E L N I A K N L V G S A M A  
2761 GATGTTTCCGCATTGGTTGAGTTGAACATTGCTAAGAATTTGGTTGGATCTGCAATGGCT 2820

G S V G G F N A H A A N L V T A V F L A  
2821 GGGTCTGTTGGTGGATTTAACGCACATGCAGCTAATTTAGTGACAGCTGTTTTCTTGGCA 2880

L G Q D P A Q N V E S S N C I T L M K E  
2881 TTAGGACAAGATCCTGCACAAAATGTTGAAAGTTCCAACCTGTATAACATTGATGAAAGAA 2940

V D G D L R I S V S M P S I E V G T I G  
2941 GTGGACGGTGATTTGAGAATTTCCGTATCCATGCCATCCATCGAAGTAGGTACCATCGGT 3000

G G T V L E P Q G A M L D L L G V R G P  
3001 GGTGGTACTGTTCTAGAACCAAGGTGCCATGTTGGACTTATTAGGTGTAAGAGGCCCCG 3060

H A T A P G T N A R Q L A R I V A C A V  
3061 CATGCTACCGCTCCTGGTACCAACGCACGTCAATTAGCAAGAATAGTTGCCTGTGCCGTC 3120

L A G E L S L C A A L A A G H L V Q S H  
3121 TTGGCAGGTGAATTATCCTTATGTGCTGCCCTAGCAGCCGCCATTTGGTTCAAAGTCAT 3180

M T H N R K P A E P T K P N N L D A T D  
3181 ATGACCCACAACAGGAAACCTGCTGAACCAACAAAACCTAACAATTTGGACGCCACTGAT 3240

I N R L K D G S V T C I K S \*  
3241 ATAAATCGTTTGAAAGATGGGTCCGTCACCTGCATTAAATCCTAAACTTAGTCATACGTC 3300

3301 ATTGGTATTCTCTTGAAAAAGAAGCACAACAGCACCATGTGTTACGTAAAATATTTACTT 3360

FIG. 2<sub>CONT'D</sub>

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## FIG. 3

## Arabidopsis HMGR1

1 ATCAGCCACCTCACCACCTCTCTCCTCTCTCCTCTCTCTCCCCCTGGAGAGATTATTC 60  
M D L R R R P P K P P V T N N N N  
61 ATTCCCTCCAATGGATCTCCGTCGGAGGCCTCCTAAACCACCGTTACCAACAACAACAA 120  
S N G S F R S Y Q P R T S D D D H R R R  
121 CTCCAACGGATCTTTCCGTTCTTATCAGCCTCGCACTTCCGATGACGATCATCGTCGCCG 180  
A T T I A P P P K A S D A L P L P L Y L  
181 GGCTACAACAATTGCTCCTCCACCGAAAGCATCCGACGCGCTTCCTCTTCCGTTATATCT 240  
T N A V F F T L F F S V A Y Y L L H R W  
241 CACAAACGCCGTTTTCTTCACGCTCTTCTTCTCCGTCGCGTATTACCTCCTCCACCGGTG 300  
R D K I R Y N T P L H V V T I T E L G A  
301 GCGTGACAAGATCCGTTACAATACGCCTCTTCACGTCGTCCTACTATCACAGAACTCGGCGC 360  
I I A L I A S F I Y L L G F F G I D F V  
361 CATTATTGCTCTCATCGCTTCGTTTATCTATCTCCTAGGGTTTTTTGGTATTGACTTTGT 420  
Q S F I S R A S G D A W D L A D T I D D  
421 TCAGTCATTTATCTCACGTGCCTCTGGTGATGCTTGGGATCTCGCCGATACGATCGATGA 480  
D D H R L V T C S P P T P I V S V A K L  
481 TGATGACCACCGCCTTGTCACGTGCTCTCCACCGACTCCGATCGTTTCCGTTGCTAAATT 540  
P N P E P I V T E S L P E E D E E I V K  
541 ACCTAATCCGGAACCTATTGTTACCGAATCGCTTCCTGAGGAAGACGAGGAGATTGTGAA 600  
S V I D G V I P S Y S L E S R L G D C K  
601 ATCGGTTATCGACGGAGTTATTCCATCGTACTCGCTTGAATCTCGTCTCGGTGATTGCAA 660  
R A A S I R R E A L Q R V T G R S I E G  
661 AAGAGCGGCGTCGATTGCTCGTGAGGCGTTGCAGAGAGTCACCGGGAGATCGATTGAAGG 720  
L P L D G F D Y E S I L G Q C C E M P V  
721 GTTACCGTTGGATGGATTTGATTATGAATCGATTTTGGGGCAATGCTGTGAGATGCCTGT 780  
G Y I Q I P V G I A G P L L L D G Y E Y  
781 TGGATACATTGAGATTCCCTGTTGGGATTGCTGGTCCATTGTTGCTTGATGGTTATGAGTA 840  
S V P M A T T E G C L V A S T N R G C K  
841 CTCTGTTCCATGGCTACAACCGAAGGTTGTTTGGTTGCTAGCTAACAGAGGCTGCAA 900  
A M F I S G G A T S T V L K D G M T R A  
901 GGCTATGTTTATCTCTGGTGGCGCCACAGTACCGTTCTTAAGGACGGTATGACCCGAGC 960  
P V V R F A S A R R A S E L K F F L E N  
961 ACCTGTTGTTCCGTTTCGCTTCGGCGAGACGAGCTTCGGAGCTTAAGTTTTTCTTGAGAA 1020  
P E N F D T L A V V F N R S S R F A R L  
1021 TCCAGAGAACTTTGATACTTTGGCAGTAGTCTTCAACAGGTCGAGTAGATTGCAAGACT 1080

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1081 Q S V K C T I A G K N A Y V R F C C S T 1140  
G C A A A G T G T T A A A T G C A C A A T C G C G G G G A A G A A T G C T T A T G T A A G G T T C T G T T G T A G T A C  
1141 G D A M G M N M V S K G V Q N V L E Y L 1200  
T G G T G A T G C T A T G G G G A T G A A T A T G G T T T C T A A A G G T G T G C A G A A T G T T C T T G A G T A T C T  
1201 T D D F P D M D V I G I S G N F C S D K 1260  
T A C C G A T G A T T T C C C T G A C A T G G A T G T G A T T G G A A T C T C T G G T A A C T T C T G T T C G G A C A A  
1261 K P A A V N W I E G R G K S V V C E A V 1320  
G A A A C C T G C T G C T G T G A A C T G G A T T G A G G G A C G T G G T A A A T C A G T T G T T T G C G A G G C T G T  
1321 I R G E I V N K V L K T S V A A L V E L 1380  
A A T C A G A G G A G A G A T C G T G A A C A A G G T C T T G A A A C G A G C G T G G C T G C T T T A G T C G A G C T  
1381 N M L K N L A G S A V A G S L G G F N A 1440  
C A A C A T G C T C A A G A A C C T A G C T G G C T C T G C T G T T G C A G G C T C T C T A G G T G G A T T C A A C G C  
1441 H A S N I V S A V F I A T G Q D P A Q N 1500  
T C A T G C C A G T A A C A T A G T G T C T G C T G T A T T C A T A G C T A C T G G C C A A G A T C C A G C T C A A A A  
1501 V E S S Q C I T M M E A I N D G K D I H 1560  
C G T G G A G A G T T C T C A A T G C A T C A C C A T G A T G G A A G C T A T T A A T G A C G G C A A A G A T A T C C A  
1561 I S V T M P S I E V G T V G G G T Q L A 1620  
T A T C T C A G T C A C T A T G C C A T C T A T C G A G G T G G G G A C A G T G G G A G G A G G A A C A C A G C T T G C  
1621 S Q S A C L N L L G V K G A S T E S P G 1680  
A T C T C A A T C A G C G T G T T T A A C C T G C T C G G A G T T A A G G A G C A A G C A C A G A G T C G C C G G G  
1681 M N A R R L A T I V A G A V L A G E L S 1740  
A A T G A A C G C A A G G A G G C T A G C G A C G A T C G T A G C C G G A G C A G T T T T A G C T G G A G A G T T A T C  
1741 L M S A I A A G Q L V R S H M K Y N R S 1800  
T T T A A T G T C A G C A A T T G C A G C T G G A C A G C T T G T G A G A A G T C A C A T G A A A T A C A A T A G A T C  
1801 S R D I S G A T T T T T T T T \* 1860  
C A G C C G A G A C A T C T C T G G A G C A A C G A C A A C G A C A A C A A C A C A T G A T C T G A A T C T G A  
1861 A T C A T C A T C C T C T C A A A G A A G G A C A A C A A T C C A A A A C A A G G G C A G G C T T T T T A C A A C G C A 1920  
1921 T T C A C T C A A A A C T C G C T G G T G G A C A G A T T T T A G C C A T G T G C G T A T G C G T T T G C C C T T T T G 1980  
1981 T T A A A T A A A A A A C T A T T T G T T T T G T T T G T T T G A C T T G A T A T C T T T T T T T G G G A T T G A G G 2040  
2041 A T T G A G A G A G A T A G A G A G A T T T T A C A A A C T T T C T C T T T T C T C T T T C T C T T T C T C A 2100  
2101 T G G A T A A T T C G T G T C T C T T T G A T T T G T C T A A G G T T T G T C T T T G T T T G T T A G G A A G T G G T C 2160  
2161 T A T A T G A A C G A A A A A T T T G T G T A T G G T G C A G T T G C G T T T G G G G A C A T T T T T G A G A T T T T T 2220  
2221 T C T C T G T T T T G T T T C C T C T C T T C G T T T T T A T T G T T T G T T A C A T A T A A A A T A T T T C T C T G T 2280  
2281 A T G T T G G A A C A T C T C T C T C T T T A G T T G T T G T T G G T A A A A G A T A C G G A T C T T C T T T C C T 2340  
2341 C C A G A A G A A T C C A T C T A T A T A A T A T T A C C A T C T A T G T G T T C T A C T 2385

FIG. 3 CONT'D  
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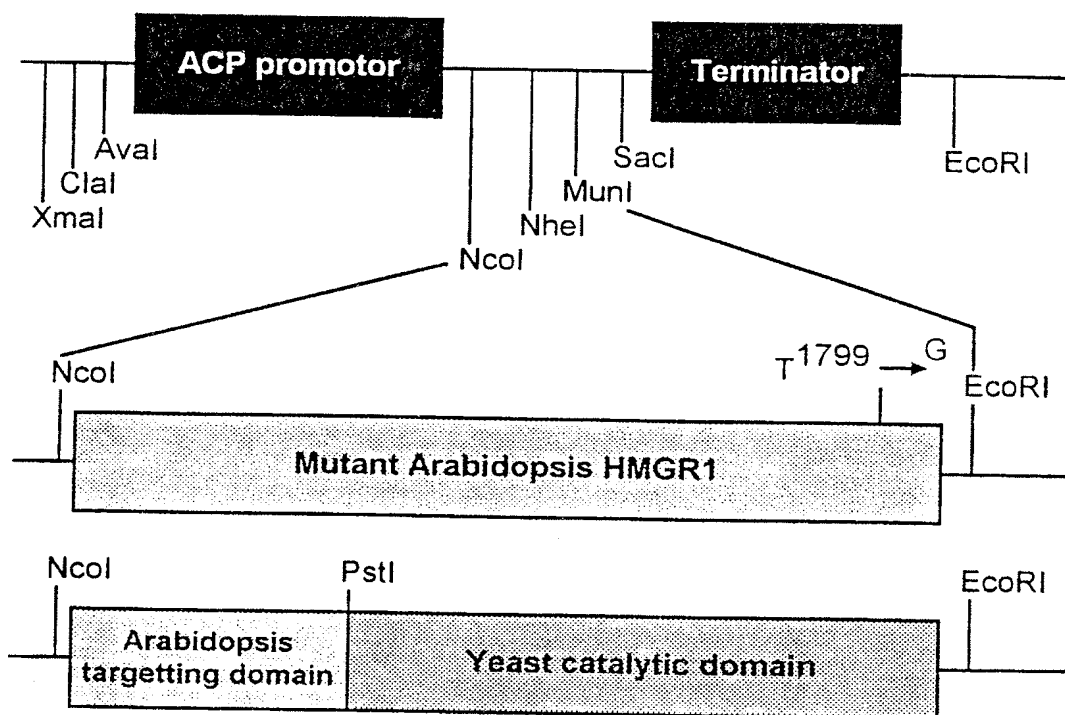


FIG. 4a

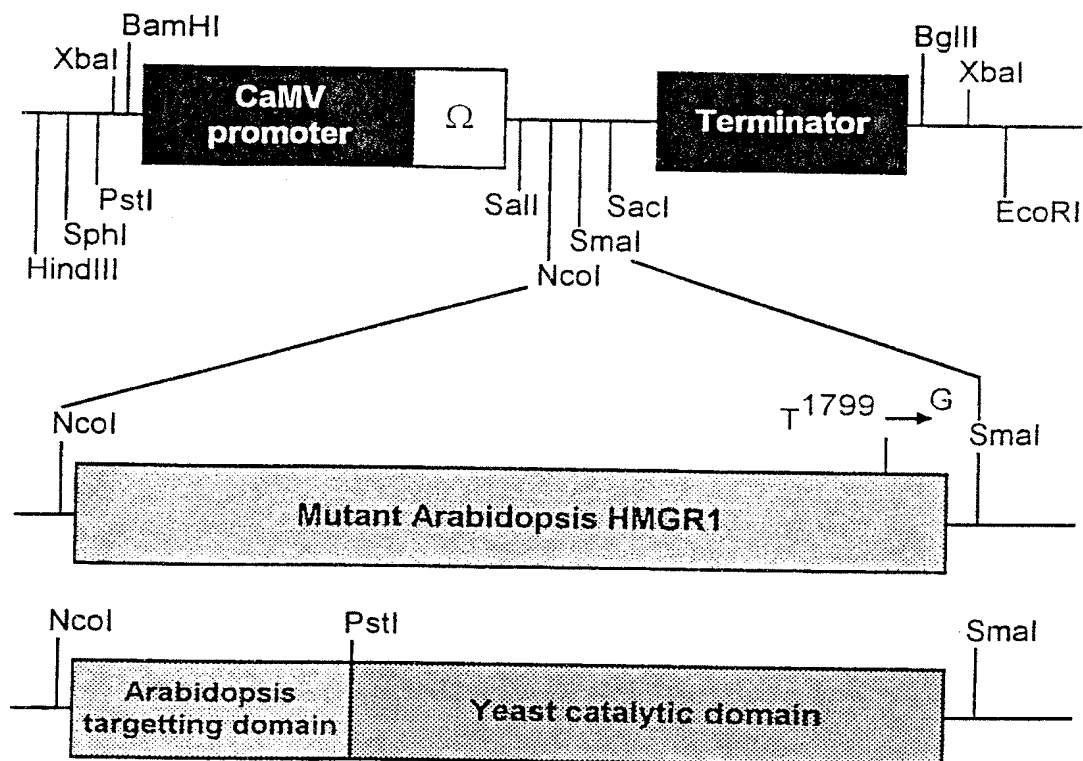


FIG. 4b

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## FIG. 5a

Nucleotide and derived amino acid sequence of a novel, mutant gene  
produced by site-directed mutagenesis of Arabidopsis HMGR1

1	M D L R R R P P K P P V T N N N N S N G	
	CCATGGATCTCCGTCGGAGGCCTCCTAAACCACCGGTTACCAACAACAACACTCCAACG	60
61	S F R S Y Q P R T S D D D H R R R A T T	
	GATCTTTCCGTTCTTATCAGCCTCGCACTTCCGATGACGATCATCGTCGCCGGGGCTACAA	120
121	I A P P P K A S D A L P L P L Y L T N A	
	CAATTGCTCCTCCACCGAAAGCATCCGACGCGCTTCTCTTCCGTTATATCTCACAAACG	180
181	V F F T L F F S V A Y Y L L H R W R D K	
	CCGTTTTCTTCACGCTCTTCTTCTCCGTCGCGTATTACCTCCTCCACCGGTGGCGTGACA	240
241	I R Y N T P L H V V T I T E L G A I I A	
	AGATCCGTTACAATACGCCTCTTCACGTCGTCACACTATCACAGAACTCGGCGCCATTATTG	300
301	L I A S F I Y L L G F F G I D F V Q S F	
	CTCTCATCGCTTCGTTTATCTATCTCCTAGGGTTTTTTGGTATTGACTTTGTTTCAGTCAT	360
361	I S R A S G D A W D L A D T I D D D D H	
	TTATCTCACGTGCCTCTGGTGATGCTTGGGATCTCGCCGATACGATCGATGATGATGACC	420
421	R L V T C S P P T P I V S V A K L P N P	
	ACCGCCTTGTACGTGCTCTCCACCGACTCCGATCGTTTTCCGTTGCTAAATTACCTAATC	480
481	E P I V T E S L P E E D E E I V K S V I	
	CGGAACCTATTGTTACCGAATCGCTTCTGAGGAAGACGAGGAGATTGTGAAATCGGTTA	540
541	D G V I P S Y S L E S R L G D C K R A A	
	TCGACGGAGTTATTCCATCGTACTCGCTTGAATCTCGTCTCGGTGATTGCAAAAGAGCGG	600
601	S I R R E A L Q R V T G R S I E G L P L	
	CGTCGATTTCGTGAGGCGTTGCAGAGAGTCACCGGGAGATCGATTGAAGGGTTACCGT	660
661	D G F D Y E S I L G Q C C E M P V G Y I	
	TGGATGGATTTGATTATGAATCGATTTTGGGGCAATGCTGTGAGATGCCTGTTGGATACA	720
721	Q I P V G I A G P L L L D G Y E Y S V P	
	TTCAGATTCCTGTTGGGATTGCTGGTCCATTGTTGCTTGATGGTTATGAGTACTCTGTTC	780
781	M A T T E G C L V A S T N R G C K A M F	
	CTATGGCTACAACCGAAGGTTGTTTGGTTGCTAGCACTAACAGAGGCTGCAAGGCTATGT	840

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841 I S G G A T S T V L K D G M T R A P V V  
TTATCTCTGGTGGCGCCACCAGTACCGTTCTTAAGGACGGTATGACCCGAGCACCTGTTG 900

901 R F A S A R R A S E L K F F L E N P E N  
TTCGGTTCGCTTCGGCGAGACGAGCTTCGGAGCTTAAGTTTTCTTGGAGAATCCAGAGA 960

961 F D T L A V V F N R S S R F A R L Q S V  
ACTTTGATACTTTGGCAGTAGTCTTCAACAGGTGAGTAGATTGCAAGACTGCAAAGTG 1020

1021 K C T I A G K N A Y V R F C C S T G D A  
TTAAATGCACAATCGCGGGGAAGAATGCTTATGTAAGGTTCTGTTGTAGTACTGGTGATG 1080

1081 M G M N M V S K G V Q N V L E Y L T D D  
CTATGGGGATGAATATGGTTTCTAAAGGTGTGCAGAATGTTCTTGAGTATCTTACCGATG 1140

1141 F P D M D V I G I S G N F C S D K K P A  
ATTTCCCTGACATGGATGTGATTGGAATCTCTGGTAACTTCTGTTCCGACAAGAAACCTG 1200

1201 A V N W I E G R G K S V V C E A V I R G  
CTGCTGTGAACTGGATTGAGGGACGTGGTAAATCAGTTGTTTGCAGGGCTGTAATCAGAG 1260

1261 E I V N K V L K T S V A A L V E L N M L  
GAGAGATCGTGAACAAGGTCTTGAAAACGAGCGTGGCTGCTTTAGTCGAGCTCAACATGC 1320

1321 K N L A G S A V A G S L G G F N A H A S  
TCAAGAACCTAGCTGGCTCTGCTGTTGCAGGCTCTCTAGGTGGATTCAACGCTCATGCCA 1380

1381 N I V S A V F I A T G Q D P A Q N V E S  
GTAACATAGTGTCTGCTGTATTCTAGCTACTGGCCAAGATCCAGCTCAAACGTGGAGA 1440

1441 S Q C I T M M E A I N D G K D I H I S V  
GTTCTCAATGCATCACCATGATGGAAGCTATTAATGACGGCAAAGATATCCATATCTCAG 1500

1501 T M P S I E V G T V G G G T Q L A S Q S  
TCACTATGCCATCTATCGAGGTGGGGACAGTGGGAGGAGGAACACAGCTTGCATCTCAAT 1560

1561 A C L N L L G V K G A S T E S P G M N A  
CAGCGTGTTTAAACCTGCTCGGAGTTAAAGGAGCAAGCACAGAGTCGCCGGAATGAACG 1620

1621 R R L A T I V A G A V L A G E L S L M S  
CAAGGAGGCTAGCGACGATCGTAGCCGAGCAGTTTTAGCTGGAGAGTTATCTTTAATGT 1680

1681 A I A A G Q L V R S H M K Y N R A S R D  
CAGCAATTGCAGCTGGACAGCTTGTGAGAAGTCACATGAAATACAATAGAGCCAGCCGAG 1740

1741 I S G A T T T T T T T T \*  
ACATCTCTGGAGCAACGACAACGACAACAACAACATGATCTGAATCTGAATTC 1796

FIG. 5a<sub>CONT'D</sub>

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## FIG. 5b

Nucleotide and derived amino acid sequence of a novel sequence  
comprising part of *Arabidopsis thaliana* HMGR1 and part of yeast HMGR1

```

      M D L R R R P P K P P V T N N N N S N G
1  CCATGGATCTCCGTCGGAGGCCTCCTAAACCACCGGTTACCAACAACAACAACTCCAACG   60

      S F R S Y Q P R T S D D D H R R R A T T
61 GATCTTTCCGTTCTTATCAGCCTCGCACTTCCGATGACGATCATCGTCGCCGGGCTACAA   120

      I A P P P K A S D A L P L P L Y L T N A
121 CAATTGCTCCTCCACCGAAAGCATCCGACGCGCTTCTTCCGTTATATCTCACAAACG   180

      V F F T L F F S V A Y Y L L H R W R D K
181 CCGTTTTCTTCACGCTCTTCTTCTCCGTCGCGTATTACCTCCTCCACCGGTGGCGTGACA   240

      I R Y N T P L H V V T I T E L G A I I A
241 AGATCCGTTACAATACGCCTCTTCACGTCGTCACTATCACAGAACTCGGCGCCATTATTG   300

      L I A S F I Y L L G F F G I D F V Q S F
301 CTCTCATCGCTTCGTTTATCTATCTCCTAGGGTTTTTTGGTATTGACTTTGTTTCAGTCAT   360

      I S R A S G D A W D L A D T I D D D D H
361 TTATCTCACGTGCCTCTGGTGATGCTTGGGATCTCGCCGATACGATCGATGATGATGACC   420

      R L V T C S P P T P I V S V A K L P N P
421 ACCGCCTTGTCACGTGCTCTCCACCGACTCCGATCGTTTCCGTTGCTAAATTACCTAATC   480

      Arabidopsis ←      → Yeast

      E P I V T E S L P A E N K E V A A L V I
481 CGGAACCTATTGTTACCGAATCGCTTCCTGCAGAGAACAAAGAGGTCGCTGCCTTGGTTA   540

      H G K L P L Y A L E K K L G D T T R A V
541 TTCACGGTAAGTTACCTTTGTACGCTTTGGAGAAAAAATTAGGTGATACTACGAGAGCGG   600

      A V R R K A L S I L A E A P V L A S D R
601 TTGCGGTACGTAGGAAGGCTCTTCAATTTTGGCAGAAGCTCCTGTATTAGCATCTGATC   660

      L P Y K N Y D Y D R V F G A C C E N V I
661 GTTTACCATATAAAAATTATGACTACGACCGCGTATTTGGCGCTTGTTGTGAAAATGTTA   720

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G Y M P L P V G V I G P L V I D G T S Y  
721 TAGGTTACATGCCTTTGCCCCGTTGGTGTATAGGCCCTTGGTTATCGATGGTACATCTT 780

H I P M A T T E G C L V A S A M R G C K  
781 ATCATATACCAATGGCAACTACAGAGGGTGTGGTAGCTTCTGCCATGCGTGGCTGTA 840

A I N A G G G A T T V L T K D G M T R G  
841 AGGCAATCAATGCTGGCGGTGGTGCACAACTGTTTTAACTAAGGATGGTATGACAAGAG 900

P V V R F P T L K R S G A C K I W L D S  
901 GCCCAGTAGTCCGTTTCCCACTTTGAAAAGATCTGGTGCCTGTAAGATATGGTTAGACT 960

E E G Q N A I K K A F N S T S R F A R L  
961 CAGAAGAGGGACAAAACGCAATTAAAAAGCTTTAACTCTACATCAAGATTGTCACGTC 1020

Q H I Q T C L A G D L L F M R F R T T T  
1021 TGCAACATATTCAAACCTGTCTAGCAGGAGATTACTCTTCATGAGATTTAGAACAACATA 1080

G D A M G M N M I S K G V E Y S L K Q M  
1081 CTGGTGACGCAATGGGTATGAATATGATTTCTAAAGGTGTGCAATACTCATTAAAGCAAA 1140

V E E Y G W E D M E V V S V S G N Y C T  
1141 TGGTAGAAGAGTATGGCTGGGAAGATATGGAGGTTGTCTCCGTTTCTGGTAACTACTGTA 1200

D K K P A A I N W I E G R G K S V V A E  
1201 CCGACAAAAAACAGCTGCCATCAACTGGATCGAAGGTGCTGGTAAGAGTGTGCTGCGCAG 1260

A T I P G D V V R K V L K S D V S A L V  
1261 AAGCTACTATTCTGGTGATGTTGTGCAAAAAGTGTTAAAAAGTGATGTTTCCGCATTGG 1320

E L N I A K N L V G S A M A G S V G G F  
1321 TTGAGTTGAACATTGCTAAGAATTTGGTTGGATCTGCAATGGCTGGGTCTGTTGGTGGAT 1380

N A H A A N L V T A V F L A L G Q D P A  
1381 TTAACGCACATGCAGCTAATTTAGTGACAGCTGTTTTCTTGGCATTAGGACAAGATCCTG 1440

Q N V E S S N C I T L M K E V D G D L R  
1441 CACAAAATGTTGAAAGTTCCAAGTGTATAACATTGATGAAAGAAGTGGACGGTGATTTGA 1500

I S V S M P S I E V G T I G G G T V L E  
1501 GAATTTCCGTATCCATGCCATCCATCGAAGTAGGTACCATCGGTGGTGGTACTGTTCTAG 1560

P Q G A M L D L L G V R G P H A T A P G  
1561 AACCACAAGGTGCCATGTTGGACTTATTAGGTGTAAGAGGCCCGCATGCTACCGCTCCTG 1620

T N A R Q L A R I V A C A V L A G E L S  
1621 GTACCAACGCACGTCAATTAGCAAGAATAGTTGCCTGTGCCGTCTTGGCAGGTGAATTAT 1680

L C A A L A A G H L V Q S H M T H N R K  
1681 CCTTATGTGCTGCCCTAGCAGCCGGCCATTTGGTTCAAAGTCATATGACCCACAACAGGA 1740

P A E P T K P N N L D A T D I N R L K D  
1741 AACCTGCTGAACCAACAAAACCTAACAATTTGGACGCCACTGATATAAATCGTTTGAAAG 1800

G S V T C I K S \*  
1801 ATGGGTCCGTACCTGCATTAAATCCTAAACTTAGTCATACGTGCAATTC 1850

FIG. 5b CONT'D

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## FIG. 6

athmgr1	.....	.....	.....	.....	MD	2
athmgrm	.....	.....	.....	.....	MD	2
chimaeric	.....	.....	.....	.....	MD	2
schmgr1	NLSVVVIIMK	LSVILLFVFI	NFYNFGANWV	NDAFNSLYFG		439
athmgr1	LRRRPPKPPV	TNNNNSN...	.....	GSFRSYQP		27
athmgrm	LRRRPPKPPV	TNNNNSN...	.....	GSFRSYQP		27
chimaeric	LRRRPPKPPV	TNNNNSN...	.....	GSFRSYQP		27
schmgr1	KERVSLPDFI	TSNASENFKE	QAIVSVTPLL	YYKPIKSYQR		479
athmgr1	RTSDDDHRRR	ATTIAPPPKA	SDALPLPLYL	TNAVFETLEF		67
athmgrm	RTSDDDHRRR	ATTIAPPPKA	SDALPLPLYL	TNAVFETLEF		67
chimaeric	RTSDDDHRRR	ATTIAPPPKA	SDALPLPLYL	TNAVFETLEF		67
schmgr1	IEDMVLLLR	NVSVAIRDRF	VSKLVLSALV	CSAV.....		513
athmgr1	SVAYYLLHRW	RDKIRYNTPL	HV...VTITE	LGATIALIAS		104
athmgrm	SVAYYLLHRW	RDKIRYNTPL	HV...VTITE	LGATIALIAS		104
chimaeric	SVAYYLLHRW	RDKIRYNTPL	HV...VTITE	LGATIALIAS		104
schmgr1	.INVYLLNAA	RIHTSYTADQ	LVKTEVTKKS	FTAPVQKAST		552
athmgr1	FIYLLGFFGI	DFVQSFISSA	SGDAWDLADT	IDDDDHRLVT		144
athmgrm	FIYLLGFFGI	DFVQSFISSA	SGDAWDLADT	IDDDDHRLVT		144
chimaeric	FIYLLGFFGI	DFVQSFISSA	SGDAWDLADT	IDDDDHRLVT		144
schmgr1	PVLTNKTVIS	GSKVKSLSSA	QSSSSGPSSS	SEEDDSRDIE		592
athmgr1	CSPPTPIVSV	AKLPNPEPIV	TESLPEE...D	EEIVKSVIDG		182
athmgrm	CSPPTPIVSV	AKLPNPEPIV	TESLPEE...D	EEIVKSVIDG		182
chimaeric	CSPPTPIVSV	AKLPNPEPIV	TESLPAE...N	KEVAALVIHG		182
schmgr1	SLDK....KI	RPLEELEALL	SSGNTKQLKN	KEVAALVIHG		628
athmgr1	VIPSYSLER	LGDCKRAASI	RREALQRTVG	RSI...EGLP		219
athmgrm	VIPSYSLER	LGDCKRAASI	RREALQRTVG	RSI...EGLP		219
chimaeric	KLPLYALEKK	LGDTRAVAV	RRKALSILAE	APVLASDRLP		222
schmgr1	KLPLYALEKK	LGDTRAVAV	RRKALSILAE	APVLASDRLP		668
athmgr1	LDGFDYESIL	GQCCMPVGY	IQIPVGIAGP	LLLDGYEYSV		259
athmgrm	LDGFDYESIL	GQCCMPVGY	IQIPVGIAGP	LLLDGYEYSV		259
chimaeric	YKNYDYDRVF	GACCENVIY	MPLPVGVI GP	LVIDGTSYHI		262
schmgr1	YKNYDYDRVF	GACCENVIY	MPLPVGVI GP	LVIDGTSYHI		708

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athmgr1	PMATTEGCLV	ASTNRGCKAM	FISGGATSTV	LKDGMPTRAPV	299
athmgrm	PMATTEGCLV	ASTNRGCKAM	FISGGATSTV	LKDGMPTRAPV	299
chimaeric	PMATTEGCLV	ASTNRGCKAM	NAGGGATTVL	TKDGMPTRGPV	302
schmgr1	PMATTEGCLV	ASTNRGCKAM	NAGGGATTVL	TKDGMPTRGPV	748
athmgr1	VRFASARRAS	ELKFFLENPE	NFDTLAVVFN	RSSRFARLOS	339
athmgrm	VRFASARRAS	ELKFFLENPE	NFDTLAVVFN	RSSRFARLOS	339
chimaeric	VRFPTLKRSR	ACKIWLDSEE	GQNAIKKAFN	STSRFARLOH	342
schmgr1	VRFPTLKRSR	ACKIWLDSEE	GQNAIKKAFN	STSRFARLOH	788
athmgr1	VKCTIAGKNA	YVRFCCSTGD	AMGMNMVSKG	VQNVLEYLTD	379
athmgrm	VKCTIAGKNA	YVRFCCSTGD	AMGMNMVSKG	VQNVLEYLTD	379
chimaeric	IQTCLAGDLL	FMRFRTTTGD	AMGMNMI SKG	VEYSLKQOMVE	382
schmgr1	IQTCLAGDLL	FMRFRTTTGD	AMGMNMI SKG	VEYSLKQOMVE	828
athmgr1	DFP...DMDVI	GISGNFCS DK	KPAAVNWIEG	RGKSVVCEAV	417
athmgrm	DFP...DMDVI	GISGNFCS DK	KPAAVNWIEG	RGKSVVCEAV	417
chimaeric	EYGWEDMEVV	SVSGNYCTDK	KPAAINWIEG	RGKSVVAEAT	422
schmgr1	EYGWEDMEVV	SVSGNYCTDK	KPAAINWIEG	RGKSVVAEAT	868
athmgr1	IRGEIVNKVL	KTSVAALVEL	NMLKNLAGSA	VAGSLGGFNA	457
athmgrm	IRGEIVNKVL	KTSVAALVEL	NMLKNLAGSA	VAGSLGGFNA	457
chimaeric	IPGDVVRKVL	KSDVSALVEL	NIAKNLV GSA	MAGSVGGFNA	462
schmgr1	IPGDVVRKVL	KSDVSALVEL	NIAKNLV GSA	MAGSVGGFNA	908
athmgr1	HASNIVSAVF	IATGQDPAQN	VESSQCITMM	EAINDGKDIH	497
athmgrm	HASNIVSAVF	IATGQDPAQN	VESSQCITMM	EAINDGKDIH	497
chimaeric	HAANLVIAVF	LALGQDPAQN	VESSNCITLM	KEVDG...DLR	500
schmgr1	HAANLVIAVF	LALGQDPAQN	VESSNCITLM	KEVDG...DLR	946
athmgr1	ISVTMPSEIV	GTVGGGTQLA	SQSACLNL LG	VKGASTESPG	537
athmgrm	ISVTMPSEIV	GTVGGGTQLA	SQSACLNL LG	VKGASTESPG	537
chimaeric	ISVSMPSEIV	GTIGGGTVLE	PQGAMLDLLG	VRGPHATAPG	540
schmgr1	ISVSMPSEIV	GTIGGGTVLE	PQGAMLDLLG	VRGPHATAPG	986
athmgr1	MNARRLATIV	ACAVLAGELS	LMSAIAAGQL	VRSHMKYNRS	577
athmgrm	MNARRLATIV	ACAVLAGELS	LMSAIAAGQL	VRSHMKYNRA	577
chimaeric	TNARQLARIV	ACAVLAGELS	LCAALAAGHL	VQSHMTHNRK	580
schmgr1	TNARQLARIV	ACAVLAGELS	LCAALAAGHL	VQSHMTHNRK	1026
athmgr1	SRDISGATTT	TTTTT.....			592
athmgrm	SRDISGATTT	TTTTT.....			592
chimaeric	PAEPTKPNNL	DATDINRLKD	GSVTCIKS		608
schmgr1	PAEPTKPNNL	DATDINRLKD	GSVTCIKS		1054

FIG. 6CONT'D

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athmgr1	MDLRRRPPKP	PVTNNNNSNG	SERSYQPTS	DDDHRRRATT	40
athmgrm	MDLRRRPPKP	PVTNNNNSNG	SERSYQPTS	DDDHRRRATT	40
athmgr1	IAPPPKASDA	LPLPLYLTNA	VFFTLFFSVA	YLLHRWRDK	80
athmgrm	IAPPPKASDA	LPLPLYLTNA	VFFTLFFSVA	YLLHRWRDK	80
athmgr1	IRYNTPLHV	TITELGAI	LIASFIYLLC	FFGIDFVSF	120
athmgrm	IRYNTPLHV	TITELGAI	LIASFIYLLC	FFGIDFVSF	120
athmgr1	ISRASGDAWS	LADTIDDDH	RLVTCSPPTP	IVSVAKLPNP	160
athmgrm	ISRASGDAWS	LADTIDDDH	RLVTCSPPTP	IVSVAKLPNP	160
athmgr1	EFIVTESLPE	EDEEIVKSVI	DGVIPSYSLE	SRLGDCKRAA	200
athmgrm	EFIVTESLPE	EDEEIVKSVI	DGVIPSYSLE	SRLGDCKRAA	200
athmgr1	STRREALQV	TGRSIEGLPL	DGFDYESILG	QCCEMPVGYI	240
athmgrm	STRREALQV	TGRSIEGLPL	DGFDYESILG	QCCEMPVGYI	240
athmgr1	QIPVGIAGPL	LLDGYEYSVP	MATTEGCLVA	STNRGCKAME	280
athmgrm	QIPVGIAGPL	LLDGYEYSVP	MATTEGCLVA	STNRGCKAME	280
athmgr1	ISGGATSTVL	KDGNTRAPVV	REFASARRASE	LKFFLENPEN	320
athmgrm	ISGGATSTVL	KDGNTRAPVV	REFASARRASE	LKFFLENPEN	320
athmgr1	FDTLAVVFNR	SSREFARLQSV	KCTIAGKNAY	VRFCSTGDA	360
athmgrm	FDTLAVVFNR	SSREFARLQSV	KCTIAGKNAY	VRFCSTGDA	360
athmgr1	MGMNMVSKGV	QNVLEYLTDD	FPDMDVIGIS	GNFCSDDKKA	400
athmgrm	MGMNMVSKGV	QNVLEYLTDD	FPDMDVIGIS	GNFCSDDKKA	400
athmgr1	AVNWIEGRGK	SVVCEAVIRG	EIVNKVLKTS	VAALVELNML	440
athmgrm	AVNWIEGRGK	SVVCEAVIRG	EIVNKVLKTS	VAALVELNML	440
athmgr1	KNLAGSAVAG	SLGGFNAAHAS	NIVSAVFIAT	GQDPAQNVR	480
athmgrm	KNLAGSAVAG	SLGGFNAAHAS	NIVSAVFIAT	GQDPAQNVR	480
athmgr1	SQCITMMEAI	NDGKDIHISV	TMPSIEVGTV	GGGTQLASQS	520
athmgrm	SQCITMMEAI	NDGKDIHISV	TMPSIEVGTV	GGGTQLASQS	520
athmgr1	ACLNLLGVKG	ASTESPGMNA	RRLATIVAGA	VLAGELSLMS	560
athmgrm	ACLNLLGVKG	ASTESPGMNA	RRLATIVAGA	VLAGELSLMS	560
athmgr1	AIAAGQLVRS	HMKYNR	SRG	ISGATTTTTT	TT 592
athmgrm	AIAAGQLVRS	HMKYNR	SRG	ISGATTTTTT	TT 592

FIG. 7

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## FIG. 8

chimaeric	<b>MDLRRRPPKP</b>	<b>PVTNNNNSNG</b>	<b>SFRSYQPRTS</b>	<b>DDDHRRRATT</b>	40
schmgr1	.....	.....	.....	.....	0
athmgr1	<b>MDLRRRPPKP</b>	<b>PVTNNNNSNG</b>	<b>SFRSYQPRTS</b>	<b>DDDHRRRATT</b>	40
chimaeric	<b>IAPPPKASDA</b>	<b>LPLPLYLTNA</b>	<b>VFFTLFFSVA</b>	<b>YYLLHRWRDK</b>	80
schmgr1	.....	.....	.....	.....	0
athmgr1	<b>IAPPPKASDA</b>	<b>LPLPLYLTNA</b>	<b>VFFTLFFSVA</b>	<b>YYLLHRWRDK</b>	80
chimaeric	<b>IRYNTPLHV</b>	<b>TITELGAIIA</b>	<b>LIASFIYLLG</b>	<b>FFGIDFVQSF</b>	120
schmgr1	.....	.....	.....	.....	0
athmgr1	<b>IRYNTPLHV</b>	<b>TITELGAIIA</b>	<b>LIASFIYLLG</b>	<b>FFGIDFVQSF</b>	120
chimaeric	<b>ISRASGDAWD</b>	<b>LADTIDDDDH</b>	<b>RLVTCSPPTP</b>	<b>IVSVAKLENP</b>	160
schmgr1	.....	.....	.....	.....	0
athmgr1	<b>ISRASGDAWD</b>	<b>LADTIDDDDH</b>	<b>RLVTCSPPTP</b>	<b>IVSVAKLENP</b>	160
chimaeric	<b>EPIVTESLPA</b>	<b>ENKEVAALVI</b>	<b>HGKLPLYALE</b>	<b>KKLGDTTTRAV</b>	200
schmgr1	.....	<b>ENKEVAALVI</b>	<b>HGKLPLYALE</b>	<b>KKLGDTTTRAV</b>	646
athmgr1	<b>EPIVTESLPE</b>	<b>E</b> .....	.....	.....	171
chimaeric	<b>AVRRKALSIL</b>	<b>AEAPVLASDR</b>	<b>LPYKNYDYDR</b>	<b>VFGACCENVI</b>	240
schmgr1	<b>AVRRKALSIL</b>	<b>AEAPVLASDR</b>	<b>LPYKNYDYDR</b>	<b>VFGACCENVI</b>	686
athmgr1	.....	.....	.....	.....	171
chimaeric	<b>GYMPLPVGVI</b>	<b>GPLVIDGTSY</b>	<b>HIPMATTEGC</b>	<b>LVASAMRGCK</b>	280
schmgr1	<b>GYMPLPVGVI</b>	<b>GPLVIDGTSY</b>	<b>HIPMATTEGC</b>	<b>LVASAMRGCK</b>	726
athmgr1	.....	.....	.....	.....	171
chimaeric	<b>AINAGGGATT</b>	<b>VLTKDGMTRG</b>	<b>PVVRFP TLKR</b>	<b>SGACKIW LDS</b>	320
schmgr1	<b>AINAGGGATT</b>	<b>VLTKDGMTRG</b>	<b>PVVRFP TLKR</b>	<b>SGACKIW LDS</b>	766
athmgr1	.....	.....	.....	.....	171

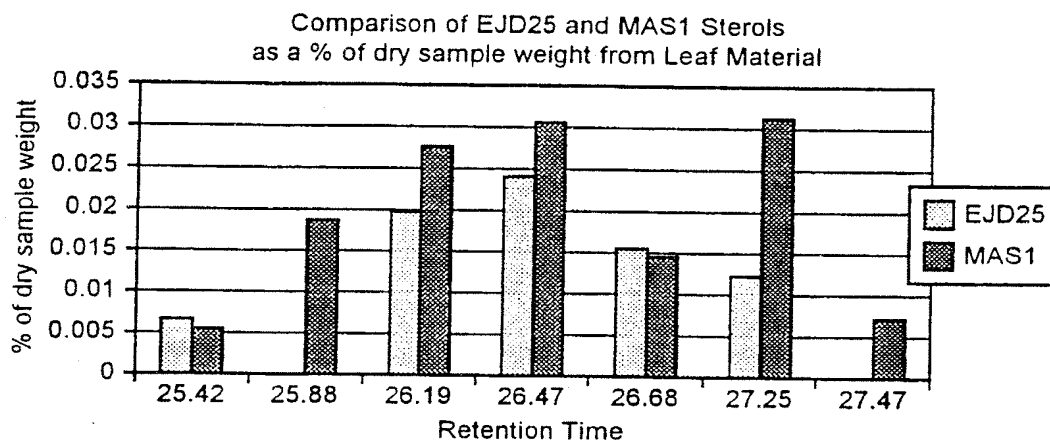
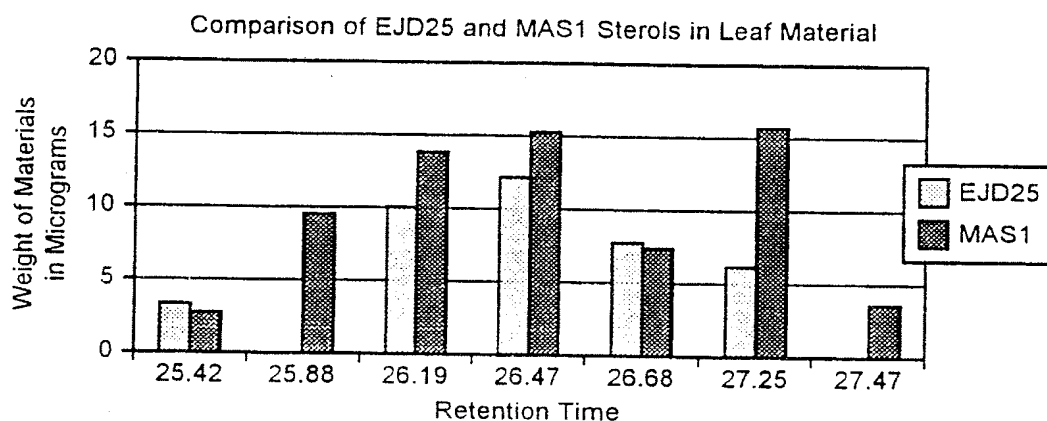
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chimaeric	<b>EEGQNAIKKA</b>	<b>FNSTSRFARL</b>	<b>QHIQTCLAGD</b>	<b>LLFMRFRITTT</b>	360
schmgr1	<b>EEGQNAIKKA</b>	<b>FNSTSRFARL</b>	<b>QHIQTCLAGD</b>	<b>LLFMRFRITTT</b>	806
athmgr1	.....	.....	.....	.....	171
chimaeric	<b>GDAMGMNMIS</b>	<b>KGVEYSLKQM</b>	<b>VEEYGWEDME</b>	<b>VVSVSGNYCT</b>	400
schmgr1	<b>GDAMGMNMIS</b>	<b>KGVEYSLKQM</b>	<b>VEEYGWEDME</b>	<b>VVSVSGNYCT</b>	846
athmgr1	.....	.....	.....	.....	171
chimaeric	<b>DKKPAAINWI</b>	<b>EGRGKSVVAE</b>	<b>ATIPGDVVRK</b>	<b>VLKSDVSALV</b>	440
schmgr1	<b>DKKPAAINWI</b>	<b>EGRGKSVVAE</b>	<b>ATIPGDVVRK</b>	<b>VLKSDVSALV</b>	886
athmgr1	.....	.....	.....	.....	171
chimaeric	<b>ELNIAKNLVG</b>	<b>SAMAGSVGGF</b>	<b>NAHAANLVTA</b>	<b>VFLALGQDPA</b>	480
schmgr1	<b>ELNIAKNLVG</b>	<b>SAMAGSVGGF</b>	<b>NAHAANLVTA</b>	<b>VFLALGQDPA</b>	926
athmgr1	.....	.....	.....	.....	171
chimaeric	<b>QNVSSNCIT</b>	<b>LMKEVDGDLR</b>	<b>ISVSMPSIEV</b>	<b>GTIGGGTVLE</b>	520
schmgr1	<b>QNVSSNCIT</b>	<b>LMKEVDGDLR</b>	<b>ISVSMPSIEV</b>	<b>GTIGGGTVLE</b>	966
athmgr1	.....	.....	.....	.....	171
chimaeric	<b>PQGAMLDLLG</b>	<b>VRGPHATAPG</b>	<b>TNARQLARIV</b>	<b>ACAVLAGELS</b>	560
schmgr1	<b>PQGAMLDLLG</b>	<b>VRGPHATAPG</b>	<b>TNARQLARIV</b>	<b>ACAVLAGELS</b>	966
athmgr1	.....	.....	.....	.....	171
chimaeric	<b>LCAALAAGHI</b>	<b>VQSHMTNRK</b>	<b>PAEPTKPNNL</b>	<b>DATDINRLKD</b>	600
schmgr1	<b>LCAALAAGHI</b>	<b>VQSHMTNRK</b>	<b>PAEPTKPNNL</b>	<b>DATDINRLKD</b>	429
athmgr1	.....	.....	.....	.....	171
chimaeric	<b>GSVTCIKS</b>	608			
schmgr1	<b>GSVTCIKS</b>	1046			
athmgr1	.....	171			

FIG. 8<sub>CONT'D</sub>

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Assignment	Retention Time	Weight			% of dry sample weight	
campesterol	25.42	3.3	2.8		0.0066	0.0056
Unknown	25.88	0	9.5		0	0.019
stigmasterol	26.19	10	13.9		0.02	0.0278
beta-sitosterol	26.47	12.1	15.3		0.0242	0.0306
iso-fucoesterol	26.68	7.76	7.4		0.0156	0.0148
Hydrocarbon	27.25	6.2	15.7		0.0124	0.0314
Hydrocarbon	27.47	0	3.6		0	0.0072
		EJD25	MAS1		EJD25	MAS1



**FIG. 9**  
SUBSTITUTE SHEET (RULE 26)

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Assignment	Retention Time		Weight			% of dry sample weight		
standard	25.19	500	500	500				
cholesterol	24.86	5.06	5.8	6.8		0.0096	0.011	0.013
campesterol	26.19	5.09	5.86	10.33		0.01	0.011	0.02
stigmasterol	26.48	4.68	6.21	6.63		0.00914	0.012	0.013
beta-sitosterol	27.27	19.86	24.46	32.6		0.0387	0.048	0.063
iso-fucoesterol	27.47	9.8	10.94	16.12		0.019	0.021	0.031
cycloartenol	28.2	0	4.12			0	0.0079	
24-ethylidene lophenol	29.31	1.92	6.01	3.92		0.00368	0.012	0.0075
		EJD25	ENH7	MAS1		EJD25	ENH7	MAS1

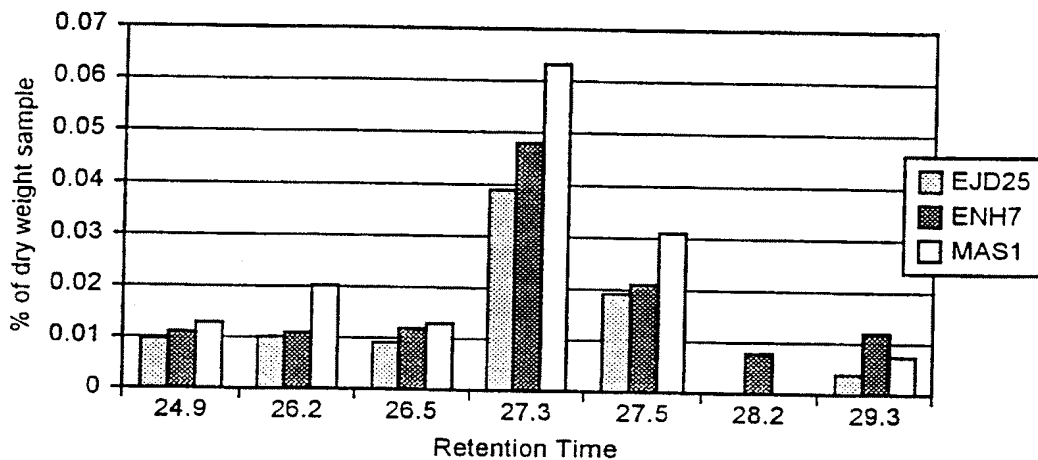
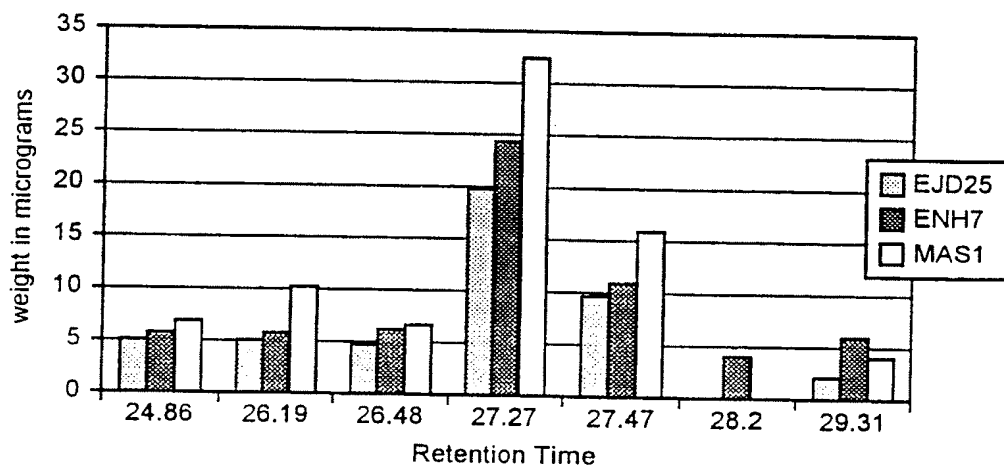


FIG. 10

SUBSTITUTE SHEET (RULE 26)



# INTERNATIONAL SEARCH REPORT

Inter. Application No

PCT/GB 00/04141

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/82 C12N15/53 C12N9/04 A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, WPI Data

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	CHAPPELL JOSEPH ET AL: "Is the reaction catalyzed by 3-hydroxy-3-methylglutaryl coenzyme A reductase a rate-limiting step for isoprenoid biosynthesis in plants?" PLANT PHYSIOLOGY, US, AMERICAN SOCIETY OF PLANT PHYSIOLOGISTS, ROCKVILLE, MD, vol. 109, no. 4, 1995, pages 1337-1343, XP002133625 ISSN: 0032-0889 the whole document	1, 4, 5, 8-10, 17-26, 28-30
X	US 5 589 619 A (WOLF FRED R ET AL) 31 December 1996 (1996-12-31)	1, 4, 5, 8-10, 17-26, 28-31, 39, 40, 43, 44
Y	the whole document	41, 42

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

12 February 2001

Date of mailing of the international search report

26/02/2001

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Maddox, A

# INTERNATIONAL SEARCH REPORT

Inter. Appl. Application No

PCT/GB 00/04141

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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Y	page 17 -page 21; tables 5,6	41,42
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International Application No

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Inter. Appl. No.

PCT/GB 00/04141

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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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A	<p>OMKUMAR RAMAKRISHNAPILLAI V ET AL:  "Phosphorylation of Ser-871 impairs the  function of His-865 of Syrian hamster  3-hydroxy-3-methylglutaryl-CoA reductase."  JOURNAL OF BIOLOGICAL CHEMISTRY,  vol. 269, no. 24, 1994, pages 16862-16866,  XP002160003  ISSN: 0021-9258  figure 1</p> <p style="text-align: center;">---</p> <p style="text-align: center;">-/--</p>	1-38

# INTERNATIONAL SEARCH REPORT

Inter national Application No

PCT/GB 00/04141

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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International Application No

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